

# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/534,424A  
Source: IFW  
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IFWO

## RAW SEQUENCE LISTING

DATE: 09/27/2006

PATENT APPLICATION: US/10/534,424A

TIME: 14:38:30

Input Set : A:\47230253.APP

Output Set: N:\CRF4\09272006\J534424A.raw

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3 <110> APPLICANT: MIYAMOTO, KAORU
4   YAMADA, KAZUYA
6 <120> TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR ZHX3
8 <130> FILE REFERENCE: 47232.5003/00US
10 <140> CURRENT APPLICATION NUMBER: 10/534,424A
11 <141> CURRENT FILING DATE: 2005-05-10
13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/09164
14 <151> PRIOR FILING DATE: 2003-07-18
16 <150> PRIOR APPLICATION NUMBER: JP 2002-366512
17 <151> PRIOR FILING DATE: 2002-12-18
19 <160> NUMBER OF SEQ ID NOS: 36
21 <170> SOFTWARE: PatentIn Ver. 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 956
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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30 1 5 10 15
32 Thr Val Val Leu Gln Asp Ala Ser Met Glu Ala Gln Pro Ala Glu Thr
33 20 25 30
35 Leu Pro Glu Gly Pro Gln Gln Asp Leu Pro Pro Glu Ala Ser Ala Ala
36 35 40 45
38 Ser Ser Glu Ala Ala Gln Asn Pro Ser Ser Thr Asp Gly Ser Thr Leu
39 50 55 60
41 Ala Asn Gly His Arg Ser Thr Leu Asp Gly Tyr Leu Tyr Ser Cys Lys
42 65 70 75 80
44 Tyr Cys Asp Phe Arg Ser His Asp Met Thr Gln Phe Val Gly His Met
45 85 90 95
47 Asn Ser Glu His Thr Asp Phe Asn Lys Asp Pro Thr Phe Val Cys Ser
48 100 105 110
50 Gly Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn
51 115 120 125
53 Ala Thr Cys His Ser Gly Glu Ala Ser Phe Val Trp Asn Val Ala Lys
54 130 135 140
56 Pro Asp Asn His Val Val Val Glu Gln Ser Ile Pro Glu Ser Thr Ser
57 145 150 155 160
59 Thr Pro Asp Leu Ala Gly Glu Pro Ser Ala Glu Gly Ala Asp Gly Gln
60 165 170 175
62 Ala Glu Ile Ile Thr Lys Thr Pro Ile Met Lys Ile Met Lys Gly
63 180 185 190
65 Lys Ala Glu Ala Lys Lys Ile His Thr Leu Lys Glu Asn Val Pro Ser
66 195 200 205

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68 Gln Pro Val Gly Glu Ala Leu Pro Lys Leu Ser Thr Gly Glu Met Glu
69      210                      215                      220
71 Val Arg Glu Gly Asp His Ser Phe Ile Asn Gly Ala Val Pro Val Ser
72 225                      230                      235                      240
74 Gln Ala Ser Ala Ser Ser Ala Lys Asn Pro His Ala Ala Asn Gly Pro
75                      245                      250                      255
77 Leu Ile Gly Thr Val Pro Val Leu Pro Ala Gly Ile Ala Gln Phe Leu
78      260                      265                      270
80 Ser Leu Gln Gln Gln Pro Pro Val His Ala Gln His His Val His Gln
81      275                      280                      285
83 Pro Leu Pro Thr Ala Lys Ala Leu Pro Lys Val Met Ile Pro Leu Ser
84      290                      295                      300
86 Ser Ile Pro Thr Tyr Asn Ala Ala Met Asp Ser Asn Ser Phe Leu Lys
87 305                      310                      315                      320
89 Asn Ser Phe His Lys Phe Pro Tyr Pro Thr Lys Ala Glu Leu Cys Tyr
90                      325                      330                      335
92 Leu Thr Val Val Thr Lys Tyr Pro Glu Glu Gln Leu Lys Ile Trp Phe
93      340                      345                      350
95 Thr Ala Gln Arg Leu Lys Gln Gly Ile Ser Trp Ser Pro Glu Glu Ile
96      355                      360                      365
98 Glu Asp Ala Arg Lys Lys Met Phe Asn Thr Val Ile Gln Ser Val Pro
99      370                      375                      380
101 Gln Pro Thr Ile Thr Val Leu Asn Thr Pro Leu Val Ala Ser Ala Gly
102 385                      390                      395                      400
104 Asn Val Gln His Leu Ile Gln Ala Ala Leu Pro Gly His Val Val Gly
105      405                      410                      415
107 Gln Pro Glu Gly Thr Gly Gly Gly Leu Leu Val Thr Gln Pro Leu Met
108      420                      425                      430
110 Ala Asn Gly Leu Gln Ala Thr Ser Ser Pro Leu Pro Leu Thr Val Thr
111      435                      440                      445
113 Ser Val Pro Lys Gln Pro Gly Val Ala Pro Ile Asn Thr Val Cys Ser
114      450                      455                      460
116 Asn Thr Thr Ser Ala Val Lys Val Val Asn Ala Ala Gln Ser Leu Leu
117 465                      470                      475                      480
119 Thr Ala Cys Pro Ser Ile Thr Ser Gln Ala Phe Leu Asp Ala Ser Ile
120      485                      490                      495
122 Tyr Lys Asn Lys Lys Ser His Glu Gln Leu Ser Ala Leu Lys Gly Ser
123      500                      505                      510
125 Phe Cys Arg Asn Gln Phe Pro Gly Gln Ser Glu Val Glu His Leu Thr
126      515                      520                      525
128 Lys Val Thr Gly Leu Ser Thr Arg Glu Val Arg Lys Trp Phe Ser Asp
129      530                      535                      540
131 Arg Arg Tyr His Cys Arg Asn Leu Lys Gly Ser Arg Ala Met Ile Pro
132 545                      550                      555                      560
134 Gly Asp His Ser Ser Ile Ile Ile Asp Ser Val Pro Glu Val Ser Phe
135      565                      570                      575
137 Ser Pro Ser Ser Lys Val Pro Glu Val Thr Cys Ile Pro Thr Thr Ala
138      580                      585                      590
140 Thr Leu Ala Thr His Pro Ser Ala Lys Arg Gln Ser Trp His Gln Thr

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141          595          600          605
143 Pro Asp Phe Thr Pro Thr Lys Tyr Lys Glu Arg Ala Pro Glu Gln Leu
144          610          615          620
146 Arg Ala Leu Glu Ser Ser Phe Ala Gln Asn Pro Leu Pro Leu Asp Glu
147 625          630          635          640
149 Glu Leu Asp Arg Leu Arg Ser Glu Thr Lys Met Thr Arg Arg Glu Ile
150          645          650          655
152 Asp Ser Trp Phe Ser Glu Arg Arg Lys Lys Val Asn Ala Glu Glu Thr
153          660          665          670
155 Lys Lys Ala Glu Glu Asn Ala Ser Gln Glu Glu Glu Glu Ala Ala Glu
156          675          680          685
158 Asp Glu Gly Gly Glu Glu Asp Leu Ala Ser Glu Leu Arg Val Ser Gly
159          690          695          700
161 Glu Asn Gly Ser Leu Glu Met Pro Ser Ser His Ile Leu Ala Glu Arg
162 705          710          715          720
164 Lys Val Ser Pro Ile Lys Ile Asn Leu Lys Asn Leu Arg Val Thr Glu
165          725          730          735
167 Ala Asn Gly Arg Asn Glu Ile Pro Gly Leu Gly Ala Cys Asp Pro Glu
168          740          745          750
170 Asp Asp Glu Ser Asn Lys Leu Ala Glu Gln Leu Pro Gly Lys Val Ser
171          755          760          765
173 Cys Lys Lys Thr Ala Gln Gln Arg His Leu Leu Arg Gln Leu Phe Val
174          770          775          780
176 Gln Thr Gln Trp Pro Ser Asn Gln Asp Tyr Asp Ser Ile Met Ala Gln
177 785          790          795          800
179 Thr Gly Leu Pro Arg Pro Glu Val Val Arg Trp Phe Gly Asp Ser Arg
180          805          810          815
182 Tyr Ala Leu Lys Asn Gly Gln Leu Lys Trp Tyr Glu Asp Tyr Lys Arg
183          820          825          830
185 Gly Asn Phe Pro Pro Gly Leu Leu Val Ile Ala Pro Gly Asn Arg Glu
186          835          840          845
188 Leu Leu Gln Asp Tyr Tyr Met Thr His Lys Met Leu Tyr Glu Glu Asp
189          850          855          860
191 Leu Gln Asn Leu Cys Asp Lys Thr Gln Met Ser Ser Gln Gln Val Lys
192 865          870          875          880
194 Gln Trp Phe Ala Glu Lys Met Gly Glu Glu Thr Arg Ala Val Ala Asp
195          885          890          895
197 Thr Gly Ser Glu Asp Gln Gly Pro Gly Thr Gly Glu Leu Thr Ala Val
198          900          905          910
200 His Lys Gly Met Gly Asp Thr Tyr Ser Glu Val Ser Glu Asn Ser Glu
201          915          920          925
203 Ser Trp Glu Pro Arg Val Pro Glu Ala Ser Ser Glu Pro Phe Asp Thr
204          930          935          940
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207 945          950          955
210 <210> SEQ ID NO: 2
211 <211> LENGTH: 522
212 <212> TYPE: PRT
213 <213> ORGANISM: Rattus norvegicus

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215 &lt;400&gt; SEQUENCE: 2

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219 Lys Cys His Ser Gly Glu Ala Ser Phe Leu Trp Asn Val Thr Lys Pro
220           20           25           30
222 Asp Asn His Val Val Val Glu Gln Ser Val Pro Glu Asn Ala Ser Ser
223           35           40           45
225 Ser Val Leu Ala Gly Glu Ser Thr Glu Gly Thr Glu Ile Ile Ile Thr
226           50           55           60
228 Lys Thr Pro Ile Met Lys Ile Met Lys Gly Lys Ala Glu Ala Lys Lys
229   65           70           75           80
231 Ile His Met Leu Lys Glu Asn Ala Pro Thr Gln Pro Gly Gly Glu Ala
232           85           90           95
234 Leu Pro Lys Pro Leu Ala Gly Glu Thr Glu Gly Lys Glu Gly Asp His
235           100          105          110
237 Thr Phe Ile Asn Gly Ala Thr Pro Val Ser Gln Ala Ser Ala Asn Ser
238           115          120          125
240 Thr Lys Pro Pro His Thr Ala Asn Gly Pro Leu Ile Gly Thr Val Pro
241           130          135          140
243 Val Leu Pro Ala Gly Ile Ala Gln Phe Leu Ser Leu Gln Gln Pro Thr
244  145          150          155          160
246 Val His Pro Gln His His Pro His Gln Pro Leu Pro Thr Ser Lys Ala
247           165          170          175
249 Leu Pro Lys Val Met Ile Pro Leu Ser Ser Ile Pro Thr Tyr Asn Ala
250           180          185          190
252 Ala Met Asp Ser Asn Ser Phe Leu Lys Asn Ser Phe His Lys Phe Pro
253           195          200          205
255 Tyr Pro Thr Lys Ala Glu Leu Cys Tyr Leu Thr Val Val Thr Lys Tyr
256           210          215          220
258 Pro Glu Glu Gln Leu Lys Ile Trp Phe Thr Ala Gln Arg Leu Lys Gln
259  225          230          235          240
261 Gly Ile Ser Trp Ser Pro Glu Glu Ile Glu Asp Ala Arg Lys Lys Met
262           245          250          255
264 Phe Asn Thr Val Ile Gln Ser Val Pro Gln Pro Thr Ile Thr Val Leu
265           260          265          270
267 Asn Thr Pro Leu Val Ala Ser Ala Gly Asn Val Gln His Leu Ile Gln
268           275          280          285
270 Ala Ala Leu Pro Gly His Ala Val Gly Gln Pro Glu Gly Thr Ala Gly
271           290          295          300
273 Gly Leu Leu Val Thr Gln Pro Leu Met Ala Asn Gly Leu Gln Ala Ser
274  305          310          315          320
276 Ser Ser Ser Leu Pro Leu Thr Thr Ala Ser Val Pro Lys Pro Thr Ala
277           325          330          335
279 Ala Pro Ile Asn Thr Val Cys Ser Asn Thr Thr Ser Ala Val Lys Val
280           340          345          350
282 Val Asn Ala Ala Gln Ser Leu Leu Thr Ala Cys Pro Ser Ile Thr Ser
283           355          360          365
285 Gln Ala Phe Leu Asp Ala Asn Ile Tyr Lys Asn Lys Lys Ser His Glu
286           370          375          380

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288 Gln Leu Ser Ala Leu Lys Gly Ser Phe Cys Arg Asn Gln Phe Pro Gly
289 385                      390                      395                      400
291 Gln Ser Glu Val Glu His Leu Thr Lys Val Thr Gly Leu Ser Thr Arg
292                      405                      410                      415
294 Glu Val Arg Lys Trp Phe Ser Asp Arg Arg Tyr His Cys Arg Asn Leu
295                      420                      425                      430
297 Lys Gly Thr Arg Ala Met Val Pro Gly Glu His Gly Ser Val Leu Ile
298                      435                      440                      445
300 Asp Ser Val Pro Glu Val Pro Phe Pro Leu Ser Ser Lys Val Pro Glu
301                      450                      455                      460
303 Val Pro Cys Val Pro Thr Ala Thr Ser Leu Val Ser His Pro Ala Thr
304 465                      470                      475                      480
306 Lys Arg Gln Ser Trp His Gln Thr Pro Asp Phe Thr Pro Thr Lys Tyr
307                      485                      490                      495
309 Lys Glu Arg Ala Pro Glu Gln Leu Arg Val Leu Glu Ser Ser Phe Ala
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318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
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322 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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325 <400> SEQUENCE: 3
326 agcttcccga attctgcag                                     19
329 <210> SEQ ID NO: 4
330 <211> LENGTH: 19
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
336     oligonucleotide
338 <400> SEQUENCE: 4
339 tcgactgcag aattcggga                                     19
342 <210> SEQ ID NO: 5
343 <211> LENGTH: 19
344 <212> TYPE: DNA
345 <213> ORGANISM: Artificial Sequence
347 <220> FEATURE:
348 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
349     oligonucleotide
351 <400> SEQUENCE: 5
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355 <210> SEQ ID NO: 6
356 <211> LENGTH: 25
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence

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**VERIFICATION SUMMARY**

DATE: 09/27/2006

PATENT APPLICATION: US/10/534,424A

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